SEQUENCE LISTING

<110> KaloBios, Inc.

<120> TRANSACTIVATION SYSTEM FOR MAMMALIAN CELLS

<130> CELA001/01WO

<160> 23

<170> PatentIn version 3.2

<210> 1
<211> 236
<212> PRT
<213> hamster

<400> 1

```
Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1               5                  10                  15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
            20                  25                  30

Gly Asp Val Asp Ala Ala Pro Leu Gly Ala Ala Pro Thr Pro Gly Ile
        35                  40                  45

Phe Ser Phe Gln Pro Glu Ser Asn Pro Thr Pro Ala Val His Arg Asp
    50                  55                  60

Met Ala Ala Arg Thr Ser Pro Leu Arg Pro Ile Val Ala Thr Thr Gly
65                  70                  75                  80

Pro Thr Leu Ser Pro Val Pro Pro Val Val His Leu Thr Leu Arg Arg
                85                  90                  95

Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met
            100                 105                 110

Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala
        115                 120                 125

Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
    130                 135                 140

Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn
145                 150                 155                 160
```

```
Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu
                165                 170                 175

Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp
            180                 185                 190

Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Val Arg Pro Leu Phe Asp
        195                 200                 205

Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly
    210                 215                 220

Ala Cys Ile Thr Leu Gly Thr Tyr Leu Gly His Lys
225                 230                 235
```

<210> 2
<211> 195
<212> PRT
<213> hamster

<400> 2

```
Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1               5                   10                  15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
            20                  25                  30

Gly Asp Val Asp Ala Ala Ala Ala Ala Ala Ser Pro Val Pro Pro Val
        35                  40                  45

Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg Tyr
    50                  55                  60

Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe
65                  70                  75                  80

Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp
                85                  90                  95

Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val
            100                 105                 110

Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn
        115                 120                 125
```

```
Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp
    130                 135                 140

Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro
145                 150                 155                 160

Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu
                165                 170                 175

Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr Leu
            180                 185                 190

Gly His Lys
        195
```

<210> 3
<211> 588
<212> DNA
<213> hamster

<400> 3

```
atggctcaag ctgggagaac agggtatgat aaccgagaga tcgtgatgaa gtacatccat     60

tataagctgt cacagagggg ctacgagtgg gatgtgggag atgtggacgc cgcggccgcg    120

gccgcgagcc ccgtgccacc tgtggtccac ctgaccctcc gccgggctgg ggatgacttc    180

tcccgtcgct accgtcgcga cttcgcggag atgtccagtc agctgcacct gacgcccttc    240

accgcgaggg gacgctttgc tacggtggtg gaggaactct tcagggatgg ggtgaactgg    300

gggaggattg tggccttctt tgagttcggt ggggtcatgt gtgtggagag cgtcaacagg    360

gagatgtcac ccctggtgga caacatcgcc ctgtggatga ccgagtacct gaaccggcat    420

ctgcacacct ggatccagga taacggaggc tgggacgcat ttgtggaact gtacggcccc    480

agtgtgaggc ctctgtttga tttctcttgg ctgtctctga agaccctgct cagcctggcc    540

ctggtcgggg cctgcatcac tctgggtacc tacctgggcc acaagtga                 588
```

<210> 4
<211> 289
<212> PRT
<213> Human adenovirus type 5

<400> 4

```
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
1               5                   10                  15
```

```
Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
            20                  25                  30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu His Asp
        35                  40                  45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
    50                  55                  60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
65                  70                  75                  80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
                85                  90                  95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
            100                 105                 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Gly His Glu Ala Gly
        115                 120                 125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu
    130                 135                 140

Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His
145                 150                 155                 160

Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met
                165                 170                 175

Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro
            180                 185                 190

Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys
        195                 200                 205

Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu
    210                 215                 220

Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro
225                 230                 235                 240
```

Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala
245 250 255

Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu
260 265 270

Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg
275 280 285

Pro

<210> 5
<211> 986
<212> DNA
<213> Human adenovirus type 5

<400> 5
atgagacata ttatctgcca cggaggtgtt attaccgaag aaatggccgc cagtcttttg 60

gaccagctga tcgaagaggt actggctgat aatcttccac ctcctagcca ttttgaacca 120

cctacccttc acgaactgca tgatttagac gtgacggccc ccgaagatcc caacgaggag 180

gcggtttcgc agatttttcc cgactctgta atgttggcgg tgcaggaagg gattgactta 240

ctcacttttc cgccggcgcc cggttctccg gagccgcctc acctttcccg gcagcccgag 300

cagccggagc agagagcctt gggtccggtt tctatgccaa accttgtacc ggaggtgatc 360

gatcttaccg gccacgaggc tggctttcca cccagtgacg acgaggatga agagggtgag 420

gagtttgtgt tagattatgt ggagcacccc gggcacggtt gcaggtcttg tcattatcac 480

cggaggaata cgggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc 540

atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggt gggtttggtg 600

tggtaatttt ttttttaatt tttacagttt tgtggtttaa agaattttgt attgtgattt 660

ttttaaaagg tcctgtgtct gaacctgagc ctgagcccga gccagaaccg gagcctgcaa 720

gacctacccg ccgtcctaaa atggcgcctg ctatcctgag acgcccgaca tcacctgtgt 780

ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg 840

agatacaccc ggtggtcccg ctgtgcccca ttaaaccagt tgccgtgaga gttggtgggc 900

gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa cctttggact 960

tgagctgtaa acgccccagg ccataa 986

<210> 6

<211> 39
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 6
cccgaattcg ccgccaccat gagacatatt atctgccac 39

<210> 7
<211> 28
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 7
cccgtcgacc ttatggcctg gggcgttt 28

<210> 8
<211> 39
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 8
cccggtaccg ccgccaccat gagacatatt atctgccac 39

<210> 9
<211> 30
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 9
cccgcggccg ccttatggcc tggggcgttt 30

<210> 10
<211> 25
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 10
ggaggtgatc gatcttaccg gccac 25

<210> 11
<211> 36
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 11
cctacccttc acgaactgca tgatttagac gtgacg 36

<210> 12
<211> 36
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 12
cgtcacgtct aaatcatgca gttcgtgaag ggtagg 36

<210> 13
<211> 38
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 13
cccgaattcg ccgccaccat ggaggcttgg gagtgttt 38

<210> 14
<211> 29
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 14
cccgtcgacc aacattcatt cccgagggt 29

<210> 15
<211> 558
<212> DNA
<213> Human adenovirus type 5

<400> 15
gaattcgccg ccaccatgga ggcttgggag tgtttggaag atttttctgc tgtgcgtaac 60

ttgctggaac agagctctaa cagtacctct tggttttgga ggtttctgtg gggctcatcc 120

caggcaaagt tagtctgcag aattaaggag gattacaagt gggaatttga agagcttttg 180

aaatcctgtg gtgagctgtt tgattctttg aatctgggtc accaggcgct tttccaagag 240

aaggtcatca agactttgga ttttttccaca ccggggcgcg ctgcggctgc tgttgctttt 300

ttgagtttta taaaggataa atggagcgaa gaaacccatc tgagcggggg gtacctgctg 360

gattttctgg ccatgcatct gtggagagcg gttgtgagac acaagaatcg cctgctactg 420

ttgtcttccg tccgcccggc gataataccg acggaggagc agcagcagca gcaggaggaa 480

gccaggcggc ggcggcagga gcagagccca tggaacccga gagccggcct ggaccctcgg 540

gaatgaatgt tggtcgac 558

<210> 16
<211> 38
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 16
cccgtcgacg ccgccaccat gccgcccaaa acccccg 38

<210> 17
<211> 32
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 17
cccgcggccg ccggtcctga gatcctcatt tc 32

<210> 18
<211> 2824
<212> DNA
<213> Homo sapiens

<400> 18
gtcgacgccg ccaccatgcc gcccaaaacc ccccgaaaaa cggccgccac cgccgccgct 60

gccgccgcgg aacccccggc accgccgccg ccgccccctc ctgaggagga cccagagcag 120

gacagcggcc cggaggacct gcctctcgtc aggcttgagt ttgaagaaac agaagaacct 180

gattttactg cattatgtca gaaattaaag ataccagatc atgtcagaga gagagcttgg 240

ttaacttggg agaaagtttc atctgtggat ggagtattgg gaggttatat tcaaaagaaa 300

aaggaactgt ggggaatctg tatctttatt gcacgagttg acctagatga gatgtcgttc 360

actttactga gctacagaaa aacatacgaa atcagtgtcc ataaattctt taacttacta 420

aaagaaattg ataccagtac caaagttgat aatgctatgt caagactgtt gaagaagtat 480

gatgtattgt ttgcactctt cagcaaattg gaaaggacat gtgaacttat atatttgaca 540

caacccagca gttcgatatc tactgaaata aattctgcat tggtgctaaa agtttcttgg 600

atcacatttt tattagctaa aggggaagta ttacaaatgg aagatgatct ggtgatttca 660

tttcagttaa tgctatgtgt ccttgactat tttattaaac tctcacctcc catgttgctc 720

aaagaaccat ataaaacagc tgttataccc attaatggtt cacctcgaac acccaggcga 780

ggtcagaaca ggagtgcacg gatagcaaaa caactagaaa atgatacaag aattattgaa 840

gttctctgta aagaacatga atgtaatata gatgaggtga aaaatgttta tttcaaaaat 900

tttatacctt ttatgaattc tcttggactt gtaacatcta atggacttcc agaggttgaa 960

aatctttcta aacgatacga agaaatttat cttaaaaata aagatctaga tcgaagatta 1020

tttttggatc atgataaaac tcttcagact gattctatag acagttttga aacacagaga 1080

acaccacgaa aaagtaacct tgatgaagag gtgaatataa ttcctccaca cactccagtt 1140

aggactgtta tgaacactat ccaacaatta atgatgattt taaattctgc aagtgatcaa 1200

ccttcagaaa atctgatttc ctattttaac aactgcacag tgaatccaaa agaaagtata 1260

ctgaaaagag tgaaggatat aggatacatc tttaaagaga aatttgctaa agctgtggga 1320

cagggttgtg tcgaaattgg atcacagcga tacaaacttg gagttcgctt gtattaccga 1380

gtaatggaat ccatgcttaa atcagaagaa gaacgattat ccattcaaaa ttttagcaaa 1440

cttctgaatg acaacatttt tcatatgtct ttattggcgt gcgctcttga ggttgtaatg 1500

gccacatata gcagaagtac atctcagaat cttgattctg gaacagattt gtctttccca 1560

tggattctga atgtgcttaa tttaaaagcc tttgattttt acaaagtgat cgaaagtttt 1620

atcaaagcag aaggcaactt gacaagagaa atgataaaac atttagaacg atgtgaacat 1680

cgaatcatgg aatcccttgc atggctctca gattcacctt tatttgatct tattaaacaa 1740

tcaaaggacc gagaaggacc aactgatcac cttgaatctg cttgtcctct taatcttcct 1800

ctccagaata atcacactgc agcagatatg tatctttctc ctgtaagatc tccaaagaaa 1860

aaaggttcaa ctacgcgtgt aaattctact gcaaatgcag agacacaagc aacctcagcc 1920

ttccagaccc agaagccatt gaaatctacc tctctttcac tgttttataa aaaagtgtat 1980

cggctagcct atctccggct aaatacactt tgtgaacgcc ttctgtctga gcacccagaa 2040

ttagaacata tcatctggac ccttttccag cacaccctgc agaatgagta tgaactcatg 2100

agagacaggc atttggacca aattatgatg tgttccatgt atggcatatg caaagtgaag 2160

aatatagacc ttaaattcaa aatcattgta acagcataca aggatcttcc tcatgctgtt 2220

caggagacat tcaaacgtgt tttgatcaaa gaagaggagt atgattctat tatagtattc 2280

tataactcgg tcttcatgca gagactgaaa acaaatattt tgcagtatgc ttccaccagg 2340

ccccctacct tgtcaccaat acctcacatt cctcgaagcc cttacaagtt tcctagttca 2400

cccttacgga ttcctggagg gaacatctat atttcacccc tgaagagtcc atataaaatt 2460

tcagaaggtc tgccaacacc aacaaaaatg actccaagat caagaatctt agtatcaatt 2520

ggtgaatcat tcgggacttc tgagaagttc cagaaaataa atcagatggt atgtaacagc 2580

gaccgtgtgc tcaaaagaag tgctgaagga agcaaccctc ctaaaccact gaaaaaacta 2640

cgctttgata ttgaaggatc agatgaagca gatggaagta aacatctccc aggagagtcc 2700

aaatttcagc agaaactggc agaaatgact tctactcgaa cacgaatgca aaagcagaaa 2760

atgaatgata gcatggatac ctcaaacaag gaagagaaat gaggatctca ggaccggcgg 2820

ccgc 2824

<210> 19
<211> 928
<212> PRT
<213> Homo sapiens

<400> 19

Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
1 5 10 15

Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp
20 25 30

Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
35 40 45

Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
50 55 60

Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65 70 75 80

Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
85 90 95

```
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Arg Val Asp Leu Asp Glu
            100                 105                 110

Met Ser Phe Thr Leu Leu Ser Tyr Arg Lys Thr Tyr Glu Ile Ser Val
        115                 120                 125

His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
    130                 135                 140

Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145                 150                 155                 160

Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
                165                 170                 175

Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
            180                 185                 190

Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
        195                 200                 205

Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
    210                 215                 220

Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
225                 230                 235                 240

Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
                245                 250                 255

Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
            260                 265                 270

Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
        275                 280                 285

Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
    290                 295                 300

Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
305                 310                 315                 320
```

```
Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Arg Arg Leu Phe
                325                 330                 335

Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
            340                 345                 350

Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Ile
        355                 360                 365

Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
    370                 375                 380

Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
385                 390                 395                 400

Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
                405                 410                 415

Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
            420                 425                 430

Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
        435                 440                 445

Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
    450                 455                 460

Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
465                 470                 475                 480

Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
                485                 490                 495

Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
            500                 505                 510

Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
        515                 520                 525

Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
    530                 535                 540

Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
545                 550                 555                 560
```

```
Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
                565                 570                 575

Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
            580                 585                 590

Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
        595                 600                 605

Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
    610                 615                 620

Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
625                 630                 635                 640

Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
                645                 650                 655

Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
            660                 665                 670

His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
        675                 680                 685

Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
    690                 695                 700

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
705                 710                 715                 720

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
                725                 730                 735

Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
            740                 745                 750

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
        755                 760                 765

Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
    770                 775                 780
```

```
Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
785                 790                 795                 800

Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
                805                 810                 815

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
            820                 825                 830

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
        835                 840                 845

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
    850                 855                 860

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
865                 870                 875                 880

Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
                885                 890                 895

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
            900                 905                 910

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
        915                 920                 925
```

<210> 20
<211> 1010
<212> DNA
<213> Homo sapiens

<400> 20

```
gaattcgccg ccaccatgac catggactct ggagcagaca accagcagag tggagatgca     60

gctgtaacag aagctgaaaa ccaacaaatg acagttcaag cccagccaca gattgccaca    120

ttagcccagg tatctatgcc agcagctcat gcaacatcat ctgctcccac cgtaactcta    180

gtacagctgc ccaatgggca gacagttcaa gtccatggag tcattcaggc ggcccagcca    240

tcagttattc agtctccaca agtccaaaca gttcagattt caactattgc agaaagtgaa    300

gattcacagg agtcagtgga tagtgtaact gattcccaaa agcgaaggga aattctttca    360

aggaggcctt ccttcaggaa aattttgaat gacttatctt ctgatgcacc aggagtgcca    420

aggattgaag aagagaagtc tgaagaggag gcttcagcac ctgccatcac cgctgtagcg    480
```

gtgccaacgc caatttaccg gactagcagt ggacagtata ttaccattac ccagagagga 540

gcaatacagc tggctagcaa tggtaccgat ggggtacagg gcctgcaaac attaaccatg 600

gccaatgcag cagccactca gccgggtact accattctac agtatgcaca gaccactgat 660

ggacagcaga tcttagtgcc cagcaaccaa gttgttgttc aagctgcctc tggagacgta 720

caaacatacc agattcgcac agcacccact agcactattg cccctggagt tgttatggca 780

tcctccccag cacttcctac acagcctgct gaagaagcag cacgaaagag agaggtccgt 840

ctaatgaaga acagggaagc agctcgtgag tgtcgtagaa agaagaaaga atatgtgaaa 900

tgtttagaaa acagagtggc agtgcttgaa aatcaaaaca agacattgat tgaggagcta 960

aaagcactta aggaccttta ctgccacaaa tcagattaat ttgggtcgac 1010

<210> 21
<211> 326
<212> PRT
<213> Homo sapiens

<400> 21

Met Thr Met Asp Ser Gly Ala Asp Asn Gln Gln Ser Gly Asp Ala Ala
1 5 10 15

Val Thr Glu Ala Glu Asn Gln Gln Met Thr Val Gln Ala Gln Pro Gln
20 25 30

Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala His Ala Thr Ser
35 40 45

Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn Gly Gln Thr Val
50 55 60

Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser Val Ile Gln Ser
65 70 75 80

Pro Gln Val Gln Thr Val Gln Ile Ser Thr Ile Ala Glu Ser Glu Asp
85 90 95

Ser Gln Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Ile
100 105 110

Leu Ser Arg Arg Pro Ser Phe Arg Lys Ile Leu Asn Asp Leu Ser Ser
115 120 125

```
Asp Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser Glu Glu Glu
    130                 135                 140

Ala Ser Ala Pro Ala Ile Thr Ala Val Ala Val Pro Thr Pro Ile Tyr
145                 150                 155                 160

Arg Thr Ser Ser Gly Gln Tyr Ile Thr Ile Thr Gln Arg Gly Ala Ile
                165                 170                 175

Gln Leu Ala Ser Asn Gly Thr Asp Gly Val Gln Gly Leu Gln Thr Leu
            180                 185                 190

Thr Met Ala Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr Ile Leu Gln
        195                 200                 205

Tyr Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro Ser Asn Gln
    210                 215                 220

Val Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr Gln Ile Arg
225                 230                 235                 240

Thr Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met Ala Ser Ser
                245                 250                 255

Pro Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys Arg Glu
            260                 265                 270

Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys Arg Arg Lys
        275                 280                 285

Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala Val Leu Glu
    290                 295                 300

Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys Asp Leu
305                 310                 315                 320

Tyr Cys His Lys Ser Asp
                325
```

<210> 22
<211> 43
<212> DNA
<213> Artificial

<220>

<223> primer

<400> 22
cccgaattcg ccgccaccat gaccatggac tctggagcag aca 43

<210> 23
<211> 30
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 23
gtcgacccaa attaatctga tttgtggcag 30

Primer 14: GTCAAGCAAGCTTGCCGCCACCATGAGACATATTATCTGCCACGG (SEQ ID NO: 24)

Primer 15: CGCAGTCTCGAGTTATGGCCTGGGGCGTTTACAGCTC (SEQ ID NO: 25)

Primer 16: CACCTACCCTTCACGAACTGCATGATTTAGACGTGACGGCC (SEQ ID NO: 26)

Primer 17: GGCCGTCACGTCTAAATCATGCAGTTCGTGAAGGGTAGGTG (SEQ ID NO: 27)

Primer 18: CGGAGGTGATCGATCTTACCGGCCACGAGGCTGGCTTTCCAC (SEQ ID NO: 28)

Primer 19: GTGGAAAGCCAGCCTCGTGGCCGGTAAGATCGATCACCTCCG (SEQ ID NO: 29)

Primer 20: GTCAAGCAAGCTTGCCGCCACCATGACCATGGAATCTGGAGC (SEQ ID NO: 30)

Primer 21: CGCAGTGGATCCTTAATCTGATTTGTGGCAGTAAAGG (SEQ ID NO: 31)

Primer 22: GTCATTCAAAATTTTCCTGAAGGAAGGCCTCCTTGAAAG (SEQ ID NO: 32)

Primer 23: TCTTTCAAGGAGGCCTTCCTTCAGGAAAATTTTGAATGAC (SEQ ID NO: 33)

Primer 24: GGCATTCCAAGCTTACTGTTGGTAAAGCCGCCACCATGGAGGCTTGGG AGTGTTTGG (SEQ ID NO: 34)

Primer 25: GATCGACTCTAGATCATTCCCGAGGGTCCAGGCCGG (SEQ ID NO: 35)

Primer 26: TAAAGCCACCATGGCTCAAGCTGGGAGAACAGGGTATG (SEQ ID NO: 36)

Primer 27: GATCGACTCTAGATCACTTGTGGCCCAGGTAGGTACCC (SEQ ID NO: 37)

Primer 28: GTGGGAGATGTGGACGCCGCGGCCGCGGCCGCGAGCCCCGTGCCAC CTGTGGTCC (SEQ ID NO: 38)

Primer 29: GGACCACAGGTGGCACGGGGCTCGCGGCCGCGGCCGCGGCGTCCAC ATCTCCCAC (SEQ ID NO: 39)

(From Figure 10) Nucleotide coding sequence of E1a cDNA (SEQ ID NO: 40):

1 aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac
HindIII M R H I I C H G G V I

51 cgaagaaatg gccgccagtc ttttggacca gctgatcgaa gaggtactgg
T E E M A A S L L D Q L I E E V L

101 ctgataatct tccacctcct agccattttg aaccacctac ccttcacgaa
A D N L P P P S H F E P P T L H E

151 ctgtatgatt tagacgtgac ggccccccgaa gatcccaacg aggaggcggt
L Y D L D V T A P E D P N E E A

201 ttcgcagatt tttcccgact ctgtaatgtt ggcggtgcag gaagggattg
V S Q I F P D S V M L A V Q E G I

251 acttactcac ttttccgccg gcgcccggtt ctccggagcc gcctcacctt
D L L T F P P A P G S P E P P H L

301 tcccggcagc ccgagcagcc ggagcagaga gccttgggtc cggtttctat
S R Q P E Q P E Q R A L G P V S

351 gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggctggct
M P N L V P E V I D L T C H E A G

401 ttccacccag tgacgacgag gatgaagagg gtgaggagtt tgtgttagat
F P P S D D E D E E G E E F V L D

451 tatgtggagc accccgggca cggttgcagg tcttgtcatt atcaccggag
Y V E H P G H G C R S C H Y H R

501 gaatacgggg gacccagata ttatgtgttc gctttgctat atgaggacct
R N T G D P D I M C S L C Y M R T

551 gtggcatgtt tgtctacagt cctgtgtctg aacctgagcc tgagcccgag
C G M F V Y S P V S E P E P E P E

601 ccagaaccgg agcctgcaag acctacccgc cgtcctaaaa tggcgcctgc
P E P E P A R P T R R P K M A P

651 tatcctgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta
A I L R R P T S P V S R E C N S S

701 cggatagctg tgactccggt ccttctaaca cacctcctga gatacacccg
T D S C D S G P S N T P P E I H P

751 gtggtcccgc tgtgccccat taaaccagtt gccgtgagag ttggtgggcg
V V P L C P I K P V A V R V G G

801 tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
R R Q A V E C I E D L L N E P G Q

851 ctttggactt gagctgtaaa cgccccaggc cataactcga g
P L D L S C K R P R P - *XhoI*

(From Figure 11) Nucleotide coding sequence of E1A mutant Y47H (SEQ ID NO: 41):

1 aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac
HindIII M R H I I C H G G V I

51 cgaagaaatg gccgccagtc ttttggacca gctgatcgaa gaggtactgg
T E E M A A S L L D Q L I E E V L

101 ctgataatct tccacctcct agccattttg aaccacctac ccttcacgaa
A D N L P P P S H F E P P T L H E

151 ctgcatgatt tagacgtgac ggccccgaa gatcccaacg aggaggcggt
L H D L D V T A P E D P N E E A

201 ttcgcagatt tttcccgact ctgtaatgtt ggcggtgcag gaagggattg
V S Q I F P D S V M L A V Q E G I

251 acttactcac ttttccgccg gcgcccggtt ctccggagcc gcctcacctt
D L L T F P P A P G S P E P P H L

301 tcccggcagc ccgagcagcc ggagcagaga gccttgggtc cggtttctat
S R Q P E Q P E Q R A L G P V S

351 gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggctggct

M P N L V P E V I D L T C H E A G

401 ttccacccag tgacgacgag gatgaagagg gtgaggagtt tgtgttagat
F P P S D D E D E E G E E F V L D

451 tatgtggagc accccgggca cggttgcagg tcttgtcatt atcaccggag
Y V E H P G H G C R S C H Y H R

501 gaatacgggg gacccagata ttatgtgttc gctttgctat atgaggacct
R N T G D P D I M C S L C Y M R T

551 gtggcatgtt tgtctacagt cctgtgtctg aacctgagcc tgagcccgag
C G M F V Y S P V S E P E P E P E

601 ccagaaccgg agcctgcaag acctacccgc cgtcctaaaa tggcgcctgc
P E P E P A R P T R R P K M A P

651 tatcctgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta
A I L R R P T S P V S R E C N S S

701 cggatagctg tgactccggt ccttctaaca cacctcctga gatacacccg
T D S C D S G P S N T P P E I H P

751 gtggtcccgc tgtgccccat taaaccagtt gccgtgagag ttggtgggcg
V V P L C P I K P V A V R V G G

801 tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
R R Q A V E C I E D L L N E P G Q

851 ctttggactt gagctgtaaa cgccccaggc cataactcga g
P L D L S C K R P R P - *XhoI*

(From Figure 12) Nucleotide coding sequence of hamster CREB-B cDNA (SEQ ID NO: 42):

1 aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
HindIII M T M E S G A D N Q Q

51 tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
S G D A A V T E A E N Q Q M T A Q

101 cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
A Q P Q I A T L A Q V S M P A A H

151 gcgacatcat ctgctcccac tgtaacctta gtgcagctgc ccaatgggca
A T S S A P T V T L V Q L P N G

201 gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
Q T V Q V H G V I Q A A Q P S V I

251 agtctccaca agtccaaaca gttcagtctt cctgtaagga cttaaaaaga
Q S P Q V Q T V Q S S C K D L K R

301 cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
L F S G T Q I S T I A E S E D S

351 ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
Q E S V D S V T D S Q K R R E I L

401 caaggaggcc ttcctacagg aaaattttga atgacttatc ttctgatgca

S R R P S Y R K I L N D L S S D A

451 ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
P G V P R I E E E K S E E E T S

501 ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
A P A I T T V T V P T P I Y Q T S

551 gtgggcagta tattgccatt acccagggag gagctataca gctggctaac
S G Q Y I A I T Q G G A I Q L A N

601 aatggtaccg atggggtaca gggccttcag acattaacca tgaccaatgc
N G T D G V Q G L Q T L T M T N

651 agctgccact cagccgggta ccactattct acagtatgca cagaccactg
A A A T Q P G T T I L Q Y A Q T T

701 atggacagca gattctagtg cccagcaacc aagttgttgt tcaagctgcc
D G Q Q I L V P S N Q V V V Q A A

751 tctggcgatg tacaaacata ccaaattcgt acagcaccca ctagcaccat
S G D V Q T Y Q I R T A P T S T

801 cgcccctgga gttgttatgg catcctcccc agcacttcct acgcagcctg
I A P G V V M A S S P A L P T Q P

851 ctgaagaagc agcccggaag agagaggttc gtctaatgaa gaacagggaa
A E E A A R K R E V R L M K N R E

901 gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga
A A R E C R R K K K E Y V K C L

951 gaacagagtg gcagtgcttg aaaaccaaaa caagacattg attgaggagc
E N R V A V L E N Q N K T L I E E

1001 taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
L K A L K D L Y C H K S D - *BamHI*

(From Figure 13) Nucleotide coding sequence of hamster CREB-B mutant Y134F (SEQ ID NO: 43):

1 aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
HindIII M T M E S G A D N Q Q

51 tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
S G D A A V T E A E N Q Q M T A Q

101 cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
A Q P Q I A T L A Q V S M P A A H

151 gcgacatcat ctgctcccac tgtaacctta gtgcagctgc ccaatgggca
A T S S A P T V T L V Q L P N G

201 gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
Q T V Q V H G V I Q A A Q P S V I

251 agtctccaca agtccaaaca gttcagtctt cctgtaagga cttaaaaaga
Q S P Q V Q T V Q S S C K D L K R

301 cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
L F S G T Q I S T I A E S E D S

351 ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
Q E S V D S V T D S Q K R R E I L

401 caaggaggcc ttcctccagg aaaattttga atgacttatc ttctgatgca
S R R P S F R K I L N D L S S D A

451 ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
P G V P R I E E E K S E E E T S

501 ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
A P A I T T V T V P T P I Y Q T S

551 gtgggcagta tattgccatt acccagggag gagctataca gctggctaac
S G Q Y I A I T Q G G A I Q L A N

601 aatggtaccg atggggtaca gggccttcag acattaacca tgaccaatgc
N G T D G V Q G L Q T L T M T N

651 agctgccact cagccgggta ccactattct acagtatgca cagaccactg
A A A T Q P G T T I L Q Y A Q T T

701 atggacagca gattctagtg cccagcaacc aagttgttgt tcaagctgcc
D G Q Q I L V P S N Q V V V Q A A

751 tctggcgatg tacaaacata ccaaattcgt acagcaccca ctagcaccat
S G D V Q T Y Q I R T A P T S T

801 cgcccctgga gttgttatgg catcctcccc agcacttcct acgcagcctg
I A P G V V M A S S P A L P T Q P

851 ctgaagaagc agcccggaag agagaggttc gtctaatgaa gaacagggaa
A E E A A R K R E V R L M K N R E

901 gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga
A A R E C R R K K K E Y V K C L

951 gaacagagtg gcagtgcttg aaaaccaaaa caagacattg attgaggagc
E N R V A V L E N Q N K T L I E E

1001 taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
L K A L K D L Y C H K S D - *BamHI*

(From Figure 14) Nucleotide coding sequence of E1b-19K (SEQ ID NO: 44):

1 aagcttactg ttggtaaagc cgccaccatg gaggcttggg agtgtttgga
HindIII M E A W E C L

51 agatttttct gctgtgcgta acttgctgga acagagctct aacagtacct
E D F S A V R N L L E Q S S N S T

101 cttggttttg gaggtttctg tggggctcat cccaggcaaa gttagtctgc
S W F W R F L W G S S Q A K L V C

151 agaattaagg aggattacaa gtgggaattt gaagagcttt tgaaatcctg
R I K E D Y K W E F E E L L K S

201 tggtgagctg tttgattctt tgaatctggg tcaccaggcg cttttccaag
C G E L F D S L N L G H Q A L F Q

251 agaaggtcat caagactttg gatttttcca caccggggcg cgctgcggct
E K V I K T L D F S T P G R A A A

301 gctgttgctt ttttgagttt tataaaggat aaatggagcg aagaaaccca
A V A F L S F I K D K W S E E T

351 tctgagcggg gggtacctgc tggattttct ggccatgcat ctgtggagag
H L S G G Y L L D F L A M H L W R

401 cggttgtgag acacaagaat cgcctgctac tgttgtcttc cgtccgcccg
A V V R H K N R L L L L S S V R P

451 gcgataatac cgacggagga gcagcagcag cagcaggagg aagccaggcg
A I I P T E E Q Q Q Q Q E E A R

501 gcggcggcag gagcagagcc catggaaccc gagagccggc ctggaccctc
R R R Q E Q S P W N P R A G L D P

551 gggaatgatc taga
R E - *XbaI*

(From Figure 15) Nucleotide coding sequence of hamster Bcl2 deletion mutant (SEQ ID NO: 45):

NcoI
1 ccatggctca agctgggaga acagggtatg ataaccgaga gatcgtgatg
M A Q A G R T G Y D N R E I V M

51 aagtacatcc attataagct gtcacagagg ggctacgagt gggatgtggg
K Y I H Y K L S Q R G Y E W D V

101 agatgtggac gccgcggccg cggccgcgag ccccgtgcca cctgtggtcc
G D V D A A A A A A A S P V P P V V

151 acctgaccct ccgccgggct ggggatgact tctcccgtcg ctaccgtcgc
H L T L R R A G D D F S R R Y R R

201 gacttcgcgg agatgtccag tcagctgcac ctgacgccct tcaccgcgag
D F A E M S S Q L H L T P F T A

251 gggacgcttt gctacggtgg tggaggaact cttcagggat ggggtgaact
R G R F A T V V E E L F R D G V N

301 gggggaggat tgtggccttc tttgagttcg gtggggtcat gtgtgtggag
W G R I V A F F E F G G V M C V E

351 agcgtcaaca gggagatgtc acccctggtg gacaacatcg ccctgtggat

S V N R E M S P L V D N I A L W

401 gaccgagtac ctgaaccggc atctgcacac ctggatccag gataacggag
M T E Y L N R H L H T W I Q D N G

451 gctgggacgc atttgtggaa ctgtacggcc ccagtgtgag gcctctgttt
G W D A F V E L Y G P S V R P L F

501 gatttctctt ggctgtctct gaagaccctg ctcagcctgg ccctggtcgg
D F S W L S L K T L L S L A L V

551 ggcctgcatc actctgggta cctacctggg ccacaagtga tctaga
G A C I T L G T Y L G H K - *XbaI*

Primer 30: CGCAGTACTAGTTTATGGCCTGGGGCGTTTACAGCTC (SEQ ID NO:46)

Primer 31: GAGCTATTCCAGAAGTAGTG (SEQ ID NO:47)